

DEC 06 2004

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<110> Lorens, James
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Holland, Sacha
Rigel Pharmaceuticals, Inc.

<120> Modulators of Angiogenesis and Tumorigenesis

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<211> 885

<212> PRT

<213> Homo sapiens

<220>

<223> AXL receptor tyrosine kinase (AXL), isoform 2; AXL
transforming sequence/gene; oncogene AXL

<400> 6

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Glu	Glu	Ser	Pro	Phe	Val	Gly	Asn	Pro	Gly	Asn	Ile	Thr	Gly	Ala	Arg	35	40	45	
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Pro	Glu	Val	His	Trp	Leu	Arg	Asp	Gly	Gln	Ile	Leu	Glu	Leu	Ala	Asp	65	70	75	80
Ser	Thr	Gln	Thr	Gln	Val	Pro	Leu	Gly	Glu	Asp	Glu	Gln	Asp	Asp	Trp	85	90	95	
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Pro	Glu	Asp	Arg	Thr	Val	Ala	Ala	Asn	Thr	Pro	Phe	Asn	Leu	Ser	Cys	145	150	155	160
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Trp	Ser	Leu	Pro	Val	Pro	Leu	Glu	Ala	Trp	Arg	Pro	Val	Lys	Glu	Pro	420	425	430
Ser	Thr	Pro	Ala	Phe	Ser	Trp	Pro	Trp	Trp	Tyr	Val	Leu	Leu	Gly	Ala	435	440	445
Val	Val	Ala	Ala	Ala	Cys	Val	Leu	Ile	Leu	Ala	Leu	Phe	Leu	Val	His	450	455	460
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Glu	Arg	Gly	Glu	Leu	Val	Val	Arg	Tyr	Arg	Val	Arg	Lys	Ser	Tyr	Ser	485	490	495
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Lys	Ile	Ala	Ile	Cys	Thr	Arg	Ser	Glu	Leu	Glu	Asp	Phe	Leu	Ser	Glu	565	570	575
Ala	Val	Cys	Met	Lys	Glu	Phe	Asp	His	Pro	Asn	Val	Met	Arg	Leu	Ile	580	585	590

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 <211> 266
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:tubulin
 cofactor D GH1-13-PCR-G3F1

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<210> 8

<211> 3927

<212> DNA

<213> Homo sapiens

<220>

<223> tubulin-specific chaperone d (TBCD), tubulin
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<400> 8

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<211> 1192

<212> PRT

<213> Homo sapiens

<220>

<223> beta-tubulin cofactor D

<400> 9

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35 40 45

Gly Gly Ala Glu Arg Glu Val Ala Leu Glu Arg Phe Arg Val Ile Met
50 55 60

Asp Lys Tyr Gln Glu Gln Pro His Leu Leu Asp Pro His Leu Glu Trp
65 70 75 80

Met Met Asn Leu Leu Leu Asp Ile Val Gln Asp Gln Thr Ser Pro Ala
85 90 95

Ser Leu Val His Leu Ala Phe Lys Phe Leu Tyr Ile Ile Thr Lys Val
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 Arg Gly Tyr Lys Thr Phe Leu Arg Leu Phe Pro His Glu Val Ala Asp
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 130 135 140
 Glu Ala Trp Glu Thr Arg Tyr Met Leu Leu Leu Trp Leu Ser Val Thr
 145 150 155 160
 Cys Leu Ile Pro Phe Asp Phe Ser Arg Leu Asp Gly Asn Leu Leu Thr
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 Gln Pro Gly Gln Ala Arg Met Ser Ile Met Asp Arg Ile Leu Gln Ile
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 Ala Glu Ser Tyr Leu Ile Val Ser Asp Lys Ala Arg Asp Ala Ala Ala
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 Val Leu Val Ser Arg Phe Ile Thr Arg Pro Asp Val Lys Gln Ser Lys
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 245 250 255
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 260 265 270
 Ala Ala Thr Val Leu Arg Cys Leu Asp Gly Cys Arg Leu Pro Glu Ser
 275 280 285
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 Gly Cys Arg Ser Leu Ala Ala Asn Leu Gln Leu Leu Thr Gln Gly Gln
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 Ser Glu Gln Lys Pro Leu Ile Leu Thr Glu Asp Asp Asp Glu Asp Asp
 340 345 350
 Asp Val Pro Glu Gly Val Glu Arg Val Ile Glu Gln Leu Leu Val Gly
 355 360 365
 Leu Lys Asp Lys Asp Thr Val Val Arg Trp Ser Ala Ala Lys Gly Ile
 370 375 380
 Gly Arg Met Ala Gly Arg Leu Pro Arg Ala Leu Ala Asp Asp Val Val
 385 390 395 400
 Gly Ser Val Leu Asp Cys Phe Ser Phe Gln Glu Thr Asp Lys Ala Trp
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His Gly Gly Cys Leu Ala Leu Ala Glu Leu Gly Arg Arg Gly Leu Leu
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 Leu Pro Ser Arg Leu Val Asp Val Val Ala Val Ile Leu Lys Ala Leu
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 Gln Glu Leu Lys Pro Phe Val Thr Ala Ile Ser Ser Ala Leu Val Ile
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 Gly Val Ile Arg Glu Leu Ala Ala Arg Ala Leu His Asn Leu Ala Gln
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 Gly Gln Leu Met Arg Gln Ala Val Cys Val Leu Ile Glu Lys Leu Ser
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 Leu Ser Lys Met Pro Phe Arg Gly Asp Thr Val Ile Asp Gly Trp Gln
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Cys	Ser	Glu	Tyr	Tyr	Met	Lys	Glu	Pro	Gly	Glu	Ala	Asp	Pro	Ala	Ile	740	745	750	
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Glu	Met	Thr	Arg	Cys	Gly	Phe	Ser	Leu	Ala	Leu	Gly	Ala	Leu	Pro	Gly	770	775	780	
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Val	Thr	His	Thr	Ser	Pro	Glu	Asp	Val	Ser	Phe	Ala	Glu	Ser	Arg	Arg	805	810	815	
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Val	Pro	Leu	Leu	Lys	Thr	Leu	Asp	His	Val	Leu	Thr	His	Gly	Cys	Phe	1045	1050	1055	

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 tgacgcgctg gcagccgtgg ttcttcacgc gccgcaggat gtccacgctg ccgatccagg 240
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<210> 11
 <211> 687
 <212> PRT
 <213> Homo sapiens

<220>
 <223> transglutaminase 2, protein-glutamine
 gamma-glutamyltransferase, tissue transglutaminase
 (TGase C, TGC, TGase-H)

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 Met Ala Glu Glu Leu Val Leu Glu Arg Cys Asp Leu Glu Leu Glu Thr
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Val	Arg	Arg	Gly	Gln	Pro	Phe	Trp	Leu	Thr	Leu	His	Phe	Glu	Gly	Arg	35	40	45	
Asn	Tyr	Glu	Ala	Ser	Val	Asp	Ser	Leu	Thr	Phe	Ser	Val	Val	Thr	Gly	50	55	60	
Pro	Ala	Pro	Ser	Gln	Glu	Ala	Gly	Thr	Lys	Ala	Arg	Phe	Pro	Leu	Arg	65	70	75	80
Asp	Ala	Val	Glu	Glu	Gly	Asp	Trp	Thr	Ala	Thr	Val	Val	Asp	Gln	Gln	85	90	95	
Asp	Cys	Thr	Leu	Ser	Leu	Gln	Leu	Thr	Thr	Pro	Ala	Asn	Ala	Pro	Ile	100	105	110	
Gly	Leu	Tyr	Arg	Leu	Ser	Leu	Glu	Ala	Ser	Thr	Gly	Tyr	Gln	Gly	Ser	115	120	125	
Ser	Phe	Val	Leu	Gly	His	Phe	Ile	Leu	Leu	Phe	Asn	Ala	Trp	Cys	Pro	130	135	140	
Ala	Asp	Ala	Val	Tyr	Leu	Asp	Ser	Glu	Glu	Glu	Arg	Gln	Glu	Tyr	Val	145	150	155	160
Leu	Thr	Gln	Gln	Gly	Phe	Ile	Tyr	Gln	Gly	Ser	Ala	Lys	Phe	Ile	Lys	165	170	175	
Asn	Ile	Pro	Trp	Asn	Phe	Gly	Gln	Phe	Glu	Asp	Gly	Ile	Leu	Asp	Ile	180	185	190	
Cys	Leu	Ile	Leu	Leu	Asp	Val	Asn	Pro	Lys	Phe	Leu	Lys	Asn	Ala	Gly	195	200	205	
Arg	Asp	Cys	Ser	Arg	Arg	Ser	Ser	Pro	Val	Tyr	Val	Gly	Arg	Val	Val	210	215	220	
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Trp	Asp	Asn	Asn	Tyr	Gly	Asp	Gly	Val	Ser	Pro	Met	Ser	Trp	Ile	Gly	245	250	255	
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Lys	Tyr	Gly	Gln	Cys	Trp	Val	Phe	Ala	Ala	Val	Ala	Cys	Thr	Val	Leu	275	280	285	
Arg	Cys	Leu	Gly	Ile	Pro	Thr	Arg	Val	Val	Thr	Asn	Tyr	Asn	Ser	Ala	290	295	300	
His	Asp	Gln	Asn	Ser	Asn	Leu	Leu	Ile	Glu	Tyr	Phe	Arg	Asn	Glu	Phe	305	310	315	320
Gly	Glu	Ile	Gln	Gly	Asp	Lys	Ser	Glu	Met	Ile	Trp	Asn	Phe	His	Cys	325	330	335	

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 Ser Thr Lys Tyr Asp Ala Pro Phe Val Phe Ala Glu Val Asn Ala Asp
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 645 650 655

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<210> 12

<211> 3257

<212> DNA

<213> Homo sapiens

<220>

<223> transglutaminase 2, C polypeptide,
 protein-glutamine gamma-glutamyltransferase (TGM2)
 cDNA

<400> 12

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<210> 13
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<212> PRT
<213> Homo sapiens

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<220>
<223> transglutaminase 2, C polypeptide,
      protein-glutamine-gamma-glutamyltransferase

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Val Arg Arg Gly Gln Pro Phe Trp Leu Thr Leu His Phe Glu Gly Arg
      35              40              45

Asn Tyr Gln Ala Ser Val Asp Ser Leu Thr Phe Ser Val Val Thr Gly
      50              55              60

Pro Ala Pro Ser Gln Glu Ala Gly Thr Lys Ala Arg Phe Pro Leu Arg
      65              70              75              80

Asp Ala Val Glu Glu Gly Asp Trp Thr Ala Thr Val Val Asp Gln Gln
      85              90              95

Asp Cys Thr Leu Ser Leu Gln Leu Thr Thr Pro Ala Asn Ala Pro Ile
      100             105             110

Gly Leu Tyr Arg Leu Ser Leu Glu Ala Ser Thr Gly Tyr Gln Gly Ser
      115             120             125

Ser Phe Val Leu Gly His Phe Ile Leu Leu Phe Asn Ala Trp Cys Pro
      130             135             140

Ala Asp Ala Val Tyr Leu Asp Ser Glu Glu Glu Arg Gln Glu Tyr Val
      145             150             155             160

Leu Thr Gln Gln Gly Phe Ile Tyr Gln Gly Ser Ala Lys Phe Ile Lys
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Asn Ile Pro Trp Asn Phe Gly Gln Phe Gln Asp Gly Ile Leu Asp Ile
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 Ser Gly Met Val Asn Cys Asn Asp Asp Gln Gly Val Leu Leu Gly Arg
 225 230 235 240
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 Ser Val Asp Ile Leu Arg Arg Trp Lys Asn His Gly Cys Gln Arg Val
 260 265 270
 Lys Tyr Gly Gln Cys Trp Val Phe Ala Ala Val Ala Cys Thr Val Leu
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 595 600 605
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 610 615 620
 Glu Gly Ala Gly Leu Thr Glu Glu Gln Lys Thr Val Glu Ile Pro Asp
 625 630 635 640
 Pro Val Glu Ala Gly Glu Glu Val Lys Val Arg Met Asp Leu Val Pro
 645 650 655
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<210> 14
 <211> 1781
 <212> DNA
 <213> Homo sapiens

<220>
 <223> similar to transglutaminase 2, C polypeptide,
 protein-glutamine-gamma-glutamyltransferase, clone
 MGC:1193 cDNA

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<210> 15

<211> 548

<212> PRT

<213> Homo sapiens

<220>

<223> similar to transglutaminase 2, C polypeptide,
protein-glutamine gamma-glutamyltransferase

<400> 15

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Asn Gly Arg Asp His His Thr Ala Asp Leu Cys Arg Glu Lys Leu Val
      20              25              30

Val Arg Arg Gly Gln Pro Phe Trp Leu Thr Leu His Phe Glu Gly Arg
      35              40              45

Asn Tyr Glu Ala Ser Val Asp Ser Leu Thr Phe Ser Val Val Thr Gly
      50              55              60

Pro Ala Pro Ser Gln Glu Ala Gly Thr Lys Ala Arg Phe Pro Leu Arg
      65              70              75              80

Asp Ala Val Glu Glu Gly Asp Trp Thr Ala Thr Val Val Asp Gln Gln
      85              90              95

Asp Cys Thr Leu Ser Leu Gln Leu Thr Thr Pro Ala Asn Ala Pro Ile
      100              105              110

Gly Leu Tyr Arg Leu Ser Leu Glu Ala Ser Thr Gly Tyr Gln Gly Ser
      115              120              125

Ser Phe Val Leu Gly His Phe Ile Leu Leu Phe Asn Ala Trp Cys Pro
      130              135              140

Ala Asp Ala Val Tyr Leu Asp Ser Glu Glu Glu Arg Gln Glu Tyr Val
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Leu Thr Gln Gln Gly Phe Ile Tyr Gln Gly Ser Ala Lys Phe Ile Lys
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Asn Ile Pro Trp Asn Phe Gly Gln Phe Glu Asp Gly Ile Leu Asp Ile
      180              185              190

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Trp	Asp	Asn	Asn	Tyr	Gly	Asp	Gly	Val	Ser	Pro	Met	Ser	Trp	Ile	Gly	245	250	255
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His	Asp	Gln	Asn	Ser	Asn	Leu	Leu	Ile	Glu	Tyr	Phe	Arg	Asn	Glu	Phe	305	310	315
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Arg	Asp	Glu	Arg	Glu	Asp	Ile	Thr	His	Thr	Tyr	Lys	Tyr	Pro	Glu	Gly	435	440	445
Ser	Ser	Glu	Glu	Arg	Glu	Ala	Phe	Thr	Arg	Ala	Asn	His	Leu	Asn	Lys	450	455	460
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Gln	Ser	Met	Asn	Met	Gly	Ser	Asp	Phe	Asp	Val	Phe	Ala	His	Ile	Thr	485	490	495
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Trp Ser Ile Cys
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<211> 1910

<212> DNA

<213> Homo sapiens

<220>

<223> transglutaminase cDNA

<400> 16

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<210> 17

<211> 548

<212> PRT

<213> Homo sapiens

<220>

<223> transglutaminase

<400> 17

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Asn	Gly	Arg	Asp	His	His	Thr	Ala	Asp	Leu	Cys	Arg	Glu	Lys	Leu	Val
			20					25					30		
Val	Arg	Arg	Gly	Gln	Pro	Phe	Trp	Leu	Thr	Leu	His	Phe	Glu	Gly	Arg
			35				40					45			
Asn	Tyr	Glu	Ala	Ser	Val	Asp	Ser	Leu	Thr	Phe	Ser	Val	Val	Thr	Gly
	50					55					60				
Pro	Ala	Pro	Ser	Gln	Glu	Ala	Gly	Thr	Lys	Ala	Arg	Phe	Pro	Leu	Arg
	65				70					75					80
Asp	Ala	Val	Glu	Glu	Gly	Asp	Trp	Thr	Ala	Thr	Val	Val	Asp	Gln	Gln
				85					90					95	
Asp	Cys	Thr	Leu	Ser	Leu	Gln	Leu	Thr	Thr	Pro	Ala	Asn	Ala	Pro	Ile
			100					105					110		
Gly	Leu	Tyr	Arg	Leu	Ser	Leu	Glu	Ala	Ser	Thr	Gly	Tyr	Gln	Gly	Ser
		115					120					125			
Ser	Phe	Val	Leu	Gly	His	Phe	Ile	Leu	Leu	Phe	Asn	Ala	Trp	Cys	Pro
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Ala	Asp	Ala	Val	Tyr	Leu	Asp	Ser	Glu	Glu	Glu	Arg	Gln	Glu	Tyr	Val
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Leu	Thr	Gln	Gln	Gly	Phe	Ile	Tyr	Gln	Gly	Ser	Ala	Lys	Phe	Ile	Lys
				165					170					175	
Asn	Ile	Pro	Trp	Asn	Phe	Gly	Gln	Phe	Glu	Asp	Gly	Ile	Leu	Asp	Ile
			180					185					190		
Cys	Leu	Ile	Leu	Leu	Asp	Val	Asn	Pro	Lys	Phe	Leu	Lys	Asn	Ala	Gly
	195						200					205			
Arg	Asp	Cys	Ser	Arg	Arg	Ser	Ser	Pro	Val	Tyr	Val	Gly	Arg	Val	Trp
	210					215					220				
Ser	Gly	Met	Val	Asn	Cys	Asn	Asp	Asp	Gln	Gly	Val	Leu	Leu	Gly	Arg
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Trp	Asp	Asn	Asn	Tyr	Gly	Asp	Gly	Val	Ser	Pro	Met	Ser	Trp	Ile	Gly
				245				250						255	
Ser	Val	Asp	Ile	Leu	Arg	Arg	Trp	Lys	Asn	His	Gly	Cys	Gln	Arg	Val
			260					265					270		
Lys	Tyr	Gly	Gln	Cys	Trp	Val	Phe	Ala	Ala	Val	Ala	Cys	Thr	Val	Leu
		275					280					285			
Arg	Cys	Leu	Gly	Ile	Pro	Thr	Arg	Val	Val	Thr	Asn	Tyr	Asn	Ser	Ala
	290					295					300				
His	Asp	Gln	Asn	Ser	Asn	Leu	Leu	Ile	Glu	Tyr	Phe	Arg	Asn	Glu	Phe
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```
<210> 18
<211> 671
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:cytosine
        deaminase GH1-27-PCR-G3F1
```

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atgaacaaaa	attcgaccga	tgtgaaaggc	tgtagtatgt	atgttgccct	gttcccttgt	120	
aatgaatgcg	ctaagctcat	catccaggga	ggtataaaa	aagtgatttt	cttgttttga	180	
taaataccat	gatagtgcag	aggcaactgc	tgcgaggctc	ctgtttaata	tggccggggt	240	
gaacattccg	aaattcatac	cgaagtgcag	caagattgtc	attgaactttg	attcaattaa	300	

```

cagcagaccg agtcaaaaagc ttcagtgagt tacatctcat tcaatctcca gaagattggg 360
attatcgtct tctaagaggt tgctaatgcc ttcatcttg aagttacaca taacttctta 420
ctagccagta tggcaaaaagt aggcatctta agaataataa gcctccaatc ttccttactg 480
tctctcttgt cacatggaat ctacatgtgt ttgaactatt gctttagggg tttaaaatag 540
gggagcctgt ggtggcctgg tgcacagggg ctagaacgag agtgcctccc cttcttgtgt 600
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cgatccggca g 671

```

<210> 19

<211> 178

<212> PRT

<213> Homo sapiens

<220>

<223> deoxycytidylate deaminase, dCMP deaminase (DCTD)

<400> 19

```

Met Ser Glu Val Ser Cys Lys Lys Arg Asp Asp Tyr Leu Glu Trp Pro
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Glu Tyr Phe Met Ala Val Ala Phe Leu Ser Ala Gln Arg Ser Lys Asp
      20              25              30

Pro Asn Ser Gln Val Gly Ala Cys Ile Val Asn Ser Glu Asn Lys Ile
      35              40              45

Val Gly Ile Gly Tyr Asn Gly Met Pro Asn Gly Cys Ser Asp Asp Val
      50              55              60

Leu Pro Trp Arg Arg Thr Ala Glu Asn Lys Leu Asp Thr Lys Tyr Pro
      65              70              75              80

Tyr Val Cys His Ala Glu Leu Asn Ala Ile Met Asn Lys Asn Ser Thr
      85              90              95

Asp Val Lys Gly Cys Ser Met Tyr Val Ala Leu Phe Pro Cys Asn Glu
      100             105             110

Cys Ala Lys Leu Ile Ile Gln Ala Gly Ile Lys Glu Val Ile Phe Met
      115             120             125

Ser Asp Lys Tyr His Asp Ser Asp Glu Ala Thr Ala Ala Arg Leu Leu
      130             135             140

Phe Asn Met Ala Gly Val Thr Phe Arg Lys Phe Ile Pro Lys Cys Ser
      145             150             155             160

Lys Ile Val Ile Asp Phe Asp Ser Ile Asn Ser Arg Pro Ser Gln Lys
      165             170             175

Leu Gln

```

<210> 20

<211> 1831

<212> DNA

<213> Homo sapiens

<220>

<223> dCMP deaminase (DCTD) cDNA

<400> 20

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atcgtgaatt cagaaaacaa gattgtcggg attgggtaca atgggatgcc aaatgggtgc 180
agtgatgacg tgttgccctg gagaaggaca gcagagaata agctggacac caaatacccg 240
tacgtgtgcc atgctggagct gaatgccatc atgaacaaaa attcgaccga tgtgaaaggc 300
tgtagtatgt atgtcgccct gttcccttgt aatgaatgcg ctaagctcat catccaggca 360
ggtataaaaag aagtgatttt cacgtctgat aaataccatg atagtacga ggcaactgct 420
gcgaggctcc tgtttaatat ggccgggggtg acattccgga aattcatacc gaagtgcagc 480
aagattgtca ttgacttttg ttcaattaac agcagaccga gtcaaaagct tcagtgaagt 540
acatctcatt caatctccag aagattggga ttatcgtctt ctaagagggt gctaatgcct 600
ttcatcttga agttacacat aacttcttac tagccagtat ggcaaaagta ggcattctaa 660
gaatataaag cctcaaactc tccttactgt ctctcttgtc acatggaatc tacatgtgtt 720
tgaactattg ctttaggatt taaaataggg gagcctgtgg tggcctgggtg cacagggtta 780
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```

<210> 21

<211> 178

<212> PRT

<213> Homo sapiens

<220>

<223> dCMP deaminase (DCTD)

<400> 21

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Met Ser Glu Val Ser Cys Lys Lys Arg Asp Asp Tyr Leu Glu Trp Pro
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Glu Tyr Phe Met Ala Val Ala Phe Leu Ser Ala Gln Arg Ser Lys Asp
          20                     25                     30

Pro Asn Ser Gln Val Gly Ala Cys Ile Val Asn Ser Glu Asn Lys Ile
          35                     40                     45

Val Gly Ile Gly Tyr Asn Gly Met Pro Asn Gly Cys Ser Asp Asp Val
          50                     55                     60

Leu Pro Trp Arg Arg Thr Ala Glu Asn Lys Leu Asp Thr Lys Tyr Pro
          65                     70                     75                     80

Tyr Val Cys His Ala Glu Leu Asn Ala Ile Met Asn Lys Asn Ser Thr
          85                     90                     95

```

```

Asp Val Lys Gly Cys Ser Met Tyr Val Ala Leu Phe Pro Cys Asn Glu
      100                      105                      110

Cys Ala Lys Leu Ile Ile Gln Ala Gly Ile Lys Glu Val Ile Phe Thr
      115                      120                      125

Ser Asp Lys Tyr His Asp Ser Asp Glu Ala Thr Ala Ala Arg Leu Leu
      130                      135                      140

Phe Asn Met Ala Gly Val Thr Phe Arg Lys Phe Ile Pro Lys Cys Ser
      145                      150                      155                      160

Lys Ile Val Ile Asp Phe Asp Ser Ile Asn Ser Arg Pro Ser Gln Lys
      165                      170                      175

```

Leu Gln

```

<210> 22
<211> 688
<212> DNA
<213> Artificial Sequence

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```

<220>
<223> Description of Artificial Sequence:peptidase M41
      (paraplegin) GH1-40-PCR-G3F1

```

```

<220>
<221> modified_base
<222> (1)..(688)
<223> n = g, a, c or t

```

```

<400> 22
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```

```

<210> 23
<211> 3087
<212> DNA
<213> Homo sapiens

```

```

<220>
<223> spastic paraplegia 7, paraplegin (pure and
      complicated autosomal recessive) (SPG7) cDNA

```

```

<400> 23
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ggattgttgt tgaacaaca tttagttcag aatccagtca gactctggca acttttaggt 300
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```

<210> 24

<211> 795

<212> PRT

<213> Homo sapiens

<220>

<223> paraplegin

<400> 24

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1

5

10

15

Leu Gly Ala Lys Val Pro Lys Gly Ala Leu Leu Leu Gly Pro Pro Gly
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 Cys Gly Lys Thr Leu Leu Ala Lys Ala Val Ala Thr Glu Ala Gln Val
 355 360 365
 Pro Phe Leu Ala Met Ala Gly Pro Glu Phe Val Glu Val Ile Gly Gly
 370 375 380
 Leu Gly Ala Ala Arg Val Arg Ser Leu Phe Lys Glu Ala Arg Ala Arg
 385 390 395 400
 Ala Pro Cys Ile Val Tyr Ile Asp Glu Ile Asp Ala Val Gly Lys Lys
 405 410 415
 Arg Ser Thr Thr Met Ser Gly Phe Ser Asn Thr Glu Glu Glu Gln Thr
 420 425 430
 Leu Asn Gln Leu Leu Val Glu Met Asp Gly Met Gly Thr Thr Asp His
 435 440 445
 Val Ile Val Leu Ala Ser Thr Asn Arg Ala Asp Ile Leu Asp Gly Ala
 450 455 460
 Leu Met Arg Pro Gly Arg Leu Asp Arg His Val Phe Ile Asp Leu Pro
 465 470 475 480
 Thr Leu Gln Glu Arg Arg Glu Ile Phe Glu Gln His Leu Lys Ser Leu
 485 490 495
 Lys Leu Thr Gln Ser Ser Thr Phe Tyr Ser Gln Arg Leu Ala Glu Leu
 500 505 510
 Thr Pro Gly Phe Ser Gly Ala Asp Ile Ala Asn Ile Cys Asn Glu Ala
 515 520 525
 Ala Leu His Ala Ala Arg Glu Gly His Thr Ser Val His Thr Leu Asn
 530 535 540
 Phe Glu Tyr Ala Val Glu Arg Val Leu Ala Gly Thr Ala Lys Lys Ser
 545 550 555 560
 Lys Ile Leu Ser Lys Glu Glu Gln Lys Val Val Ala Phe His Glu Ser
 565 570 575
 Gly His Ala Leu Val Gly Trp Met Leu Glu His Thr Glu Ala Val Met
 580 585 590
 Lys Val Ser Ile Thr Pro Arg Thr Asn Ala Ala Leu Gly Phe Ala Gln
 595 600 605
 Met Leu Pro Arg Asp Gln His Leu Phe Thr Lys Glu Gln Leu Phe Glu
 610 615 620
 Arg Met Cys Met Ala Leu Gly Gly Arg Ala Ser Glu Ala Leu Ser Phe
 625 630 635 640
 Asn Glu Val Thr Ser Gly Ala Gln Asp Asp Leu Arg Lys Val Thr Arg
 645 650 655

Ile Ala Tyr Ser Met Val Lys Gln Phe Gly Met Ala Pro Gly Ile Gly
 660 665 670
 Pro Ile Ser Phe Pro Glu Ala Gln Glu Gly Leu Met Gly Ile Gly Arg
 675 680 685
 Arg Pro Phe Ser Gln Gly Leu Gln Gln Met Met Asp His Glu Ala Arg
 690 695 700
 Leu Leu Val Ala Lys Ala Tyr Arg His Thr Glu Lys Val Leu Gln Asp
 705 710 715 720
 Asn Leu Asp Lys Leu Gln Ala Leu Ala Asn Ala Leu Leu Glu Lys Glu
 725 730 735
 Val Ile Asn Tyr Glu Asp Ile Glu Ala Leu Ile Gly Pro Pro Pro His
 740 745 750
 Gly Pro Lys Lys Met Ile Ala Pro Gln Arg Trp Ile Asp Ala Gln Arg
 755 760 765
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 Pro Leu Gly Gly Glu Glu Pro Thr Trp Pro Lys
 785 790 795

<210> 25
 <211> 373
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:CD13
 aminopeptidase GH1-72-PCR-G3F1

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 <213> Homo sapiens

<220>
 <223> aminopeptidase N, microsomal aminopeptidase,
 myeloid plasma membrane glycoprotein CD13 (GP150)

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Leu Leu Gly Val Ala Ala Val Cys Thr Ile Ile Ala Leu Ser Val Val
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 Tyr Ser Gln Glu Lys Asn Lys Asn Ala Asn Ser Ser Pro Val Ala Ser
 35 40 45
 Thr Thr Pro Ser Ala Ser Ala Thr Thr Asn Pro Ala Ser Ala Thr Thr
 50 55 60
 Leu Asp Gln Ser Lys Ala Trp Asn Arg Tyr Arg Leu Pro Asn Thr Leu
 65 70 75 80
 Lys Pro Asp Ser Tyr Gln Val Thr Leu Arg Pro Tyr Leu Thr Pro Asn
 85 90 95
 Asp Arg Gly Leu Tyr Val Phe Lys Gly Ser Ser Thr Val Arg Phe Thr
 100 105 110
 Cys Lys Glu Ala Thr Asp Val Ile Ile Ile His Ser Lys Lys Leu Asn
 115 120 125
 Tyr Thr Leu Ser Gln Gly His Arg Val Val Leu Arg Gly Val Gly Gly
 130 135 140
 Ser Gln Pro Pro Asp Ile Asp Lys Thr Glu Leu Val Glu Pro Thr Glu
 145 150 155 160
 Tyr Leu Val Val His Leu Lys Gly Ser Leu Val Lys Asp Ser Gln Tyr
 165 170 175
 Glu Met Asp Ser Glu Phe Glu Gly Glu Leu Ala Asp Asp Leu Ala Gly
 180 185 190
 Phe Tyr Arg Ser Glu Tyr Met Glu Gly Asn Val Arg Lys Val Val Ala
 195 200 205
 Thr Thr Gln Met Gln Ala Ala Asp Ala Arg Lys Ser Phe Pro Cys Phe
 210 215 220
 Asp Glu Pro Ala Met Lys Ala Glu Phe Asn Ile Thr Leu Ile His Pro
 225 230 235 240
 Lys Asp Leu Thr Ala Leu Ser Asn Met Leu Pro Lys Gly Pro Ser Thr
 245 250 255
 Pro Leu Pro Glu Asp Pro Asn Trp Asn Val Thr Glu Phe His Thr Thr
 260 265 270
 Pro Lys Met Ser Thr Tyr Leu Leu Ala Phe Ile Val Ser Glu Phe Asp
 275 280 285
 Tyr Val Glu Lys Gln Ala Ser Asn Gly Val Leu Ile Arg Ile Trp Ala
 290 295 300
 Arg Pro Ser Ala Ile Ala Ala Gly His Gly Asp Tyr Ala Leu Asn Val
 305 310 315 320
 Thr Gly Pro Ile Leu Asn Phe Phe Ala Gly His Tyr Asp Thr Pro Tyr
 325 330 335

Pro Leu Pro Lys Ser Asp Gln Ile Gly Leu Pro Asp Phe Asn Ala Gly
 340 345 350
 Ala Met Glu Asn Trp Gly Leu Val Thr Tyr Arg Glu Asn Ser Leu Leu
 355 360 365
 Phe Asp Pro Leu Ser Ser Ser Ser Ser Asn Lys Glu Arg Val Val Thr
 370 375 380
 Val Ile Ala His Glu Leu Ala His Gln Trp Phe Gly Asn Leu Val Thr
 385 390 395 400
 Ile Glu Trp Trp Asn Asp Leu Trp Leu Asn Glu Gly Phe Ala Ser Tyr
 405 410 415
 Val Glu Tyr Leu Gly Ala Asp Tyr Ala Glu Pro Thr Trp Asn Leu Lys
 420 425 430
 Asp Leu Met Val Leu Asn Asp Val Tyr Arg Val Met Ala Val Asp Ala
 435 440 445
 Leu Ala Ser Ser His Pro Leu Ser Thr Pro Ala Ser Glu Ile Asn Thr
 450 455 460
 Pro Ala Gln Ile Ser Glu Leu Phe Asp Ala Ile Ser Tyr Ser Lys Gly
 465 470 475 480
 Ala Ser Val Leu Arg Met Leu Ser Ser Phe Leu Ser Glu Asp Val Phe
 485 490 495
 Lys Gln Gly Leu Ala Ser Tyr Leu His Thr Phe Ala Tyr Gln Asn Thr
 500 505 510
 Ile Tyr Leu Asn Leu Trp Asp His Leu Gln Glu Ala Val Asn Asn Arg
 515 520 525
 Ser Ile Gln Leu Pro Thr Thr Glu Arg Asp Ile Met Asn Arg Trp Thr
 530 535 540
 Leu Gln Met Gly Phe Pro Val Ile Thr Val Asp Thr Ser Thr Gly Thr
 545 550 555 560
 Leu Ser Gln Glu His Phe Leu Leu Asp Pro Asp Ser Asn Val Thr Arg
 565 570 575
 Pro Ser Glu Phe Asn Tyr Val Trp Ile Val Pro Ile Thr Ser Ile Arg
 580 585 590
 Asp Gly Arg Gln Gln Gln Asp Tyr Trp Leu Met Asp Val Arg Ala Gln
 595 600 605
 Asn Asp Leu Phe Ser Thr Ser Gly Asn Glu Trp Val Leu Leu Asn Leu
 610 615 620
 Asn Val Thr Gly Tyr Tyr Arg Val Asn Tyr Asp Glu Glu Asn Trp Arg
 625 630 635 640
 Lys Ile Gln Thr Gln Leu Gln Arg Asp His Ser Ala Ile Pro Val Ile
 645 650 655

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Lys	Val	Pro	Val	Thr	Leu	Ala	Leu	Asn	Asn	Thr	Leu	Phe	Leu	Ile	Glu
			675			680						685			
Glu	Arg	Gln	Tyr	Met	Pro	Trp	Glu	Ala	Ala	Leu	Ser	Ser	Leu	Ser	Tyr
			690			695						700			
Phe	Lys	Leu	Met	Phe	Asp	Arg	Ser	Glu	Val	Tyr	Gly	Pro	Met	Lys	Asn
			705			710						715			
Tyr	Leu	Lys	Lys	Gln	Val	Thr	Pro	Leu	Phe	Ile	His	Phe	Arg	Asn	Asn
			725			730						735			
Thr	Asn	Asn	Trp	Arg	Glu	Ile	Pro	Glu	Asn	Leu	Met	Asp	Gln	Tyr	Ser
			740			745						750			
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			755			760						765			
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			770			775						780			
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			785			790						795			
Ile	Ala	Gln	Gly	Gly	Glu	Glu	Glu	Trp	Asp	Phe	Ala	Trp	Glu	Gln	Phe
			805			810						815			
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			820			825						830			
Ala	Cys	Ser	Lys	Glu	Leu	Trp	Ile	Leu	Asn	Arg	Tyr	Leu	Ser	Tyr	Thr
			835			840						845			
Leu	Asn	Pro	Asp	Leu	Ile	Arg	Lys	Gln	Asp	Ala	Thr	Ser	Thr	Ile	Ile
			850			855						860			
Ser	Ile	Thr	Asn	Asn	Val	Ile	Gly	Gln	Gly	Leu	Val	Trp	Asp	Phe	Val
			865			870						875			
Gln	Ser	Asn	Trp	Lys	Lys	Pro	Phe	Asn	Asp	Tyr	Gly	Gly	Gly	Ser	Phe
			885			890						895			
Ser	Phe	Ser	Asn	Leu	Ile	Gln	Ala	Val	Thr	Arg	Arg	Phe	Ser	Thr	Glu
			900			905						910			
Tyr	Glu	Leu	Gln	Gln	Leu	Glu	Gln	Phe	Lys	Lys	Asp	Asn	Glu	Glu	Thr
			915			920						925			
Gly	Phe	Gly	Ser	Gly	Thr	Arg	Ala	Leu	Glu	Gln	Ala	Leu	Glu	Lys	Thr
			930			935						940			
Lys	Ala	Asn	Ile	Lys	Trp	Val	Lys	Glu	Asn	Lys	Glu	Val	Val	Leu	Gln
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<210> 27
 <211> 3494
 <212> DNA
 <213> Homo sapiens

<220>
 <223> alanyl (membrane) aminopeptidase, aminopeptidase
 M, microsomal aminopeptidase, CD13, p150 (ANPEP)
 cDNA

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<210> 28
<211> 967
<212> PRT
<213> Homo sapiens

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<220>
<223> membrane alanine aminopeptidase precursor,
      aminopeptidase N, aminopeptidase M, microsomal
      aminopeptidase, alanyl (membrane) aminopeptidase

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Tyr Ser Gln Glu Lys Asn Lys Asn Ala Asn Ser Ser Pro Val Ala Ser
      35             40             45

Thr Thr Pro Ser Ala Ser Ala Thr Thr Asn Pro Ala Ser Ala Thr Thr
      50             55             60

Leu Asp Gln Ser Lys Ala Trp Asn Arg Tyr Arg Leu Pro Asn Thr Leu
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Lys Pro Asp Ser Tyr Gln Val Thr Leu Arg Pro Tyr Leu Thr Pro Asn
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Asp Arg Gly Leu Tyr Val Phe Lys Gly Ser Ser Thr Val Arg Phe Thr
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Cys Lys Glu Ala Thr Asp Val Ile Ile Ile His Ser Lys Lys Leu Asn
      115            120            125

Tyr Thr Leu Ser Gln Gly His Arg Val Val Leu Arg Gly Val Gly Gly
      130            135            140

Ser Gln Pro Pro Asp Ile Asp Lys Thr Glu Leu Val Glu Pro Thr Glu
      145            150            155            160

Tyr Leu Val Val His Leu Lys Gly Ser Leu Val Lys Asp Ser Gln Tyr
      165            170            175

Glu Met Asp Ser Glu Phe Glu Gly Glu Leu Ala Asp Asp Leu Ala Gly
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Phe Tyr Arg Ser Glu Tyr Met Glu Gly Asn Val Arg Lys Val Val Ala
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Pro	Lys	Met	Ser	Thr	Tyr	Leu	Leu	Ala	Phe	Ile	Val	Ser	Glu	Phe	Asp
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Tyr	Val	Glu	Lys	Gln	Ala	Ser	Asn	Gly	Val	Leu	Ile	Arg	Ile	Trp	Ala
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305					310					315					320
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				325					330					335	
Pro	Leu	Pro	Lys	Ser	Asp	Gln	Ile	Gly	Leu	Pro	Asp	Phe	Asn	Ala	Gly
			340					345					350		
Ala	Met	Glu	Asn	Trp	Gly	Leu	Val	Thr	Tyr	Arg	Glu	Asn	Ser	Leu	Leu
		355					360					365			
Phe	Asp	Pro	Leu	Ser	Ser	Ser	Ser	Ser	Asn	Lys	Glu	Arg	Val	Val	Thr
370						375					380				
Val	Ile	Ala	His	Glu	Leu	Ala	His	Gln	Trp	Phe	Gly	Asn	Leu	Val	Thr
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Ile	Glu	Trp	Trp	Asn	Asp	Leu	Trp	Leu	Asn	Glu	Gly	Phe	Ala	Ser	Tyr
				405					410					415	
Val	Glu	Tyr	Leu	Gly	Ala	Asp	Tyr	Ala	Glu	Pro	Thr	Trp	Asn	Leu	Lys
			420					425					430		
Asp	Leu	Met	Val	Leu	Asn	Asp	Val	Tyr	Arg	Val	Met	Ala	Val	Asp	Ala
		435					440					445			
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450						455					460				
Pro	Ala	Gln	Ile	Ser	Glu	Leu	Phe	Asp	Ala	Ile	Ser	Tyr	Ser	Lys	Gly
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Ala	Ser	Val	Leu	Arg	Met	Leu	Ser	Ser	Phe	Leu	Ser	Glu	Asp	Val	Phe
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Lys	Gln	Gly	Leu	Ala	Ser	Tyr	Leu	His	Thr	Phe	Ala	Tyr	Gln	Asn	Thr
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Ile	Tyr	Leu	Asn	Leu	Trp	Asp	His	Leu	Gln	Glu	Ala	Val	Asn	Asn	Arg
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 Pro Ser Glu Phe Asn Tyr Val Trp Ile Val Pro Ile Thr Ser Ile Arg
 580 585 590
 Asp Gly Arg Gln Gln Gln Asp Tyr Trp Leu Ile Asp Val Arg Ala Gln
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 Ser Ile Thr Asn Asn Val Ile Gly Gln Gly Leu Val Trp Asp Phe Val
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 Ser Phe Ser Asn Leu Ile Gln Ala Val Thr Arg Arg Phe Ser Thr Glu
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 Gly Phe Gly Ser Gly Thr Arg Ala Leu Glu Gln Ala Leu Glu Lys Thr
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 <213> Artificial Sequence

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 GH1-54-PCR-G3F1

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<210> 30
 <211> 3001
 <212> DNA
 <213> Homo sapiens

<220>
 <223> protein kinase C-like 1 (PRKCL1), PRK-1 cDNA

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<210> 31

<211> 942

<212> PRT

<213> Homo sapiens

<220>

<223> protein kinase C-like 1 (PRKCL1), serine-threonine
kinase N, PRK-1

<400> 31

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Glu Gln Leu Gly Leu Ala Gly Ala Asp Leu Ala Ala Pro Gly Val Gln
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Gln Gln Leu Glu Leu Glu Arg Glu Arg Leu Arg Arg Glu Ile Arg Lys
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Glu	Leu	Lys	Leu	Lys	Glu	Gly	Ala	Glu	Asn	Leu	Arg	Arg	Ala	Thr	Thr	50	55	60
Asp	Leu	Gly	Arg	Ser	Leu	Gly	Pro	Val	Glu	Leu	Leu	Leu	Arg	Gly	Ser	65	70	75
Ser	Arg	Arg	Leu	Asp	Leu	Leu	His	Gln	Gln	Leu	Gln	Glu	Leu	His	Ala	85	90	95
His	Val	Val	Leu	Pro	Asp	Pro	Ala	Ala	Thr	His	Asp	Gly	Pro	Gln	Ser	100	105	110
Pro	Gly	Ala	Gly	Gly	Pro	Thr	Cys	Ser	Ala	Thr	Asn	Leu	Ser	Arg	Val	115	120	125
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Ala	Glu	Asn	Met	Ile	Gln	Thr	Tyr	Ser	Asn	Gly	Ser	Thr	Lys	Asp	Arg	145	150	155
Lys	Leu	Leu	Leu	Thr	Ala	Gln	Gln	Met	Leu	Gln	Asp	Ser	Lys	Thr	Lys	165	170	175
Ile	Asp	Ile	Ile	Arg	Met	Gln	Leu	Arg	Arg	Ala	Leu	Gln	Ala	Asp	Gln	180	185	190
Leu	Glu	Asn	Gln	Ala	Ala	Pro	Asp	Asp	Thr	Gln	Gly	Ser	Pro	Asp	Leu	195	200	205
Gly	Ala	Val	Glu	Leu	Arg	Ile	Glu	Glu	Leu	Arg	His	His	Phe	Arg	Val	210	215	220
Glu	His	Ala	Val	Ala	Glu	Gly	Ala	Lys	Asn	Val	Leu	Arg	Leu	Leu	Ser	225	230	235
Ala	Ala	Lys	Ala	Pro	Asp	Arg	Lys	Ala	Val	Ser	Glu	Ala	Gln	Glu	Lys	245	250	255
Leu	Thr	Glu	Ser	Asn	Gln	Lys	Leu	Gly	Leu	Leu	Arg	Glu	Ala	Leu	Glu	260	265	270
Arg	Arg	Leu	Gly	Glu	Leu	Pro	Ala	Asp	His	Pro	Lys	Gly	Arg	Leu	Leu	275	280	285
Arg	Glu	Glu	Leu	Ala	Ala	Ala	Ser	Ser	Ala	Ala	Phe	Ser	Thr	Arg	Leu	290	295	300
Ala	Gly	Pro	Phe	Pro	Ala	Thr	His	Tyr	Ser	Thr	Leu	Cys	Lys	Pro	Ala	305	310	315
Pro	Leu	Thr	Gly	Thr	Leu	Glu	Val	Arg	Val	Val	Gly	Cys	Arg	Asp	Leu	325	330	335
Pro	Glu	Thr	Ile	Pro	Trp	Asn	Pro	Thr	Pro	Ser	Met	Gly	Gly	Pro	Gly	340	345	350
Thr	Pro	Asp	Ser	Arg	Pro	Pro	Phe	Leu	Ser	Arg	Pro	Ala	Arg	Gly	Leu	355	360	365

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 405 410 415
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 Val Phe Trp Arg Asp Gln Arg Gly Leu Cys Ala Leu Lys Phe Leu Lys
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 Glu Pro Gln Gly Cys Leu Val Ala Glu Val Thr Phe Arg Asn Pro Val
 465 470 475 480
 Ile Glu Arg Ile Pro Arg Leu Arg Arg Gln Lys Lys Ile Phe Ser Lys
 485 490 495
 Gln Gln Gly Lys Ala Phe Gln Arg Ala Arg Gln Met Asn Ile Asp Val
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 515 520 525
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 Glu Val Leu Thr Asp Thr Ser Tyr Thr Arg Ala Val Asp Trp Trp Gly
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 Ala Leu Leu Ala Arg Arg Leu Pro Pro Pro Phe Val Pro Thr Leu Ser
 885 890 895
 Gly Arg Thr Asp Val Ser Asn Phe Asp Glu Glu Phe Thr Gly Glu Ala
 900 905 910
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<210> 32

<211> 454

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Zip kinase
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aggcggccga atgcgcctgt tcagcccgga gaggtttgcg ggtagttgcc ggacattcgg 180
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cactgtgtgc ccttctcgcc gagggcggtc cccccgcgtg tgggggtgcc tgctgcggac 360
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gatctgaggt ctgatactca ctgactgttc gtaa 454

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<210> 33

<211> 2105

<212> DNA

<213> Homo sapiens

<220>

<223> death-associated protein kinase 3 (DAPK3) cDNA

<400> 33

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<210> 34

<211> 454

<212> PRT

<213> Homo sapiens

<220>

<223> death-associated protein kinase 3 (DAPK3)

<400> 34

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Lys	Gly	Thr	Gly	Lys	Glu	Tyr	Ala	Ala	Lys	Phe	Ile	Lys	Lys	Arg	Arg	35	40	45	
Leu	Ser	Ser	Ser	Arg	Arg	Gly	Val	Ser	Arg	Glu	Glu	Ile	Glu	Arg	Glu	50	55	60	
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Ser	Gly	Gly	Glu	Leu	Phe	Asp	Phe	Leu	Ala	Glu	Lys	Glu	Ser	Leu	Thr	100	105	110	
Glu	Asp	Glu	Ala	Thr	Gln	Phe	Leu	Lys	Gln	Ile	Leu	Asp	Gly	Val	His	115	120	125	
Tyr	Leu	His	Ser	Lys	Arg	Ile	Ala	His	Phe	Asp	Leu	Lys	Pro	Glu	Asn	130	135	140	
Ile	Met	Leu	Leu	Asp	Lys	Asn	Val	Pro	Asn	Pro	Arg	Ile	Lys	Leu	Ile	145	150	155	160
Asp	Phe	Gly	Ile	Ala	His	Lys	Ile	Glu	Ala	Gly	Asn	Glu	Phe	Lys	Asn	165	170	175	
Ile	Phe	Gly	Thr	Pro	Glu	Phe	Val	Ala	Pro	Glu	Ile	Val	Asn	Tyr	Glu	180	185	190	
Pro	Leu	Gly	Leu	Glu	Ala	Asp	Met	Trp	Ser	Ile	Gly	Val	Ile	Thr	Tyr	195	200	205	
Ile	Leu	Leu	Ser	Gly	Ala	Ser	Pro	Phe	Leu	Gly	Glu	Thr	Lys	Gln	Glu	210	215	220	
Thr	Leu	Thr	Asn	Ile	Ser	Ala	Val	Asn	Tyr	Asp	Phe	Asp	Glu	Glu	Tyr	225	230	235	240
Phe	Ser	Asn	Thr	Ser	Glu	Leu	Ala	Lys	Asp	Phe	Ile	Arg	Arg	Leu	Leu	245	250	255	
Val	Lys	Asp	Pro	Lys	Arg	Arg	Met	Thr	Ile	Ala	Gln	Ser	Leu	Glu	His	260	265	270	
Ser	Trp	Ile	Lys	Ala	Ile	Arg	Arg	Arg	Asn	Val	Arg	Gly	Glu	Asp	Ser	275	280	285	
Gly	Arg	Lys	Pro	Glu	Arg	Arg	Arg	Leu	Lys	Thr	Thr	Arg	Leu	Lys	Glu	290	295	300	

Tyr Thr Ile Lys Ser His Ser Ser Leu Pro Pro Asn Asn Ser Tyr Ala
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 Val Glu Ala Leu Ala Ala Ile Tyr Glu Glu Lys Glu Ala Trp Tyr Arg
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 Glu Glu Ser Asp Ser Leu Gly Gln Asp Leu Arg Arg Leu Arg Gln Glu
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 Gly Ala Leu Leu Gly Thr Ser Gly Leu Lys Arg Arg Phe Ser Arg Leu
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 Glu Asn Arg Tyr Glu Ala Leu Ala Lys Gln Val Ala Ser Glu Met Arg
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 Val Glu Cys Gly Leu Arg
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 <211> 2105
 <212> DNA
 <213> Homo sapiens

<220>
 <223> ZIP-kinase cDNA

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 <211> 454
 <212> PRT
 <213> Homo sapiens

<220>
 <223> ZIP-kinase

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 35 40 45
 Leu Ser Ser Ser Arg Arg Gly Val Ser Arg Glu Glu Ile Glu Arg Glu
 50 55 60
 Val Asn Ile Leu Arg Glu Ile Arg His Pro Asn Ile Ile Thr Leu His
 65 70 75 80
 Asp Ile Phe Glu Asn Lys Thr Asp Val Val Leu Ile Leu Glu Leu Val
 85 90 95
 Ser Gly Gly Glu Leu Phe Asp Phe Leu Ala Glu Lys Glu Ser Leu Thr
 100 105 110
 Glu Asp Glu Ala Thr Gln Phe Leu Lys Gln Ile Leu Asp Gly Val His
 115 120 125
 Tyr Leu His Ser Lys Arg Ile Ala His Phe Asp Leu Lys Pro Glu Asn
 130 135 140
 Ile Met Leu Leu Asp Lys Asn Val Pro Asn Pro Arg Ile Lys Leu Ile
 145 150 155 160
 Asp Phe Gly Ile Ala His Lys Ile Glu Ala Gly Asn Glu Phe Lys Asn
 165 170 175
 Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr Glu
 180 185 190

Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly Val Ile Thr Tyr
 195 200 205
 Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Glu Thr Lys Gln Glu
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 Thr Leu Thr Asn Ile Ser Ala Val Asn Tyr Asp Phe Asp Glu Glu Tyr
 225 230 235 240
 Phe Ser Asn Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Arg Leu Leu
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 Val Lys Asp Pro Lys Arg Arg Met Thr Ile Ala Gln Ser Leu Glu His
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 Ser Trp Ile Lys Ala Ile Arg Arg Arg Asn Val Arg Gly Glu Asp Ser
 275 280 285
 Gly Arg Lys Pro Glu Arg Arg Arg Leu Lys Thr Thr Arg Leu Lys Glu
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 Tyr Thr Ile Lys Ser His Ser Ser Leu Pro Pro Asn Asn Ser Tyr Ala
 305 310 315 320
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 Glu Gly Leu Arg Glu Leu Gln Arg Ser Arg Arg Leu Cys His Glu Asp
 340 345 350
 Val Glu Ala Leu Ala Ala Ile Tyr Glu Glu Lys Glu Ala Trp Tyr Arg
 355 360 365
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<210> 37

<211> 2055

<212> DNA

<213> Homo sapiens

<220>

<223> ZIP kinase cDNA

<400> 37

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<210> 38

<211> 454

<212> PRT

<213> Homo sapiens

<220>

<223> ZIP kinase

<400> 38

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Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Arg Lys Cys Arg Gln
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Lys Gly Thr Gly Lys Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg Arg
      35             40             45

Leu Ser Ser Ser Arg Arg Gly Val Ser Arg Glu Glu Ile Glu Arg Glu
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Val Asn Ile Leu Arg Glu Ile Arg His Pro Asn Ile Ile Thr Leu His
      65             70             75             80

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Asp	Ile	Phe	Glu	Asn	Lys	Thr	Asp	Val	Val	Leu	Ile	Leu	Glu	Leu	Val	85	90	95
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Glu	Asp	Glu	Ala	Thr	Gln	Phe	Leu	Lys	Gln	Ile	Leu	Asp	Gly	Val	His	115	120	125
Tyr	Leu	His	Ser	Lys	Arg	Ile	Ala	His	Phe	Asp	Leu	Lys	Pro	Glu	Asn	130	135	140
Ile	Met	Leu	Leu	Asp	Lys	Asn	Val	Pro	Asn	Pro	Arg	Ile	Lys	Leu	Ile	145	150	155
Asp	Phe	Gly	Ile	Ala	His	Lys	Ile	Glu	Ala	Gly	Asn	Glu	Phe	Lys	Asn	165	170	175
Ile	Phe	Gly	Thr	Pro	Glu	Phe	Val	Ala	Pro	Glu	Ile	Val	Asn	Tyr	Glu	180	185	190
Pro	Leu	Gly	Leu	Glu	Ala	Asp	Met	Trp	Ser	Ile	Gly	Val	Ile	Thr	Tyr	195	200	205
Ile	Leu	Leu	Ser	Gly	Ala	Ser	Pro	Phe	Leu	Gly	Glu	Thr	Lys	Gln	Glu	210	215	220
Thr	Leu	Thr	Asn	Ile	Ser	Ala	Val	Asn	Tyr	Asp	Phe	Asp	Glu	Glu	Tyr	225	230	235
Phe	Ser	Asn	Thr	Ser	Glu	Leu	Ala	Lys	Asp	Phe	Ile	Arg	Arg	Leu	Leu	245	250	255
Val	Lys	Asp	Pro	Lys	Arg	Arg	Met	Thr	Ile	Ala	Gln	Ser	Leu	Glu	His	260	265	270
Ser	Trp	Ile	Lys	Ala	Ile	Arg	Arg	Arg	Asn	Val	Arg	Gly	Glu	Asp	Ser	275	280	285
Gly	Arg	Lys	Pro	Glu	Arg	Arg	Arg	Leu	Lys	Thr	Thr	Arg	Leu	Lys	Glu	290	295	300
Tyr	Thr	Ile	Lys	Ser	His	Ser	Ser	Leu	Pro	Pro	Asn	Asn	Ser	Tyr	Ala	305	310	315
Asp	Phe	Glu	Arg	Phe	Ser	Lys	Val	Leu	Glu	Glu	Ala	Ala	Ala	Ala	Glu	325	330	335
Glu	Gly	Leu	Arg	Glu	Leu	Gln	Arg	Ser	Arg	Arg	Leu	Cys	His	Glu	Asp	340	345	350
Val	Glu	Ala	Leu	Ala	Ala	Ile	Tyr	Glu	Glu	Lys	Glu	Ala	Trp	Tyr	Arg	355	360	365
Glu	Glu	Ser	Asp	Ser	Leu	Gly	Gln	Asp	Leu	Arg	Arg	Leu	Arg	Gln	Glu	370	375	380
Leu	Leu	Lys	Thr	Glu	Ala	Leu	Lys	Arg	Gln	Ala	Gln	Glu	Glu	Ala	Lys	385	390	395

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<220>
<223> Description of Artificial Sequence:Gas6
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<210> 40
<211> 2461
<212> DNA
<213> Homo sapiens
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<220>
<223> growth arrest-specific 6 (GAS6) cDNA

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<210> 41

<211> 678

<212> PRT

<213> Homo sapiens

<220>

<223> growth arrest-specific 6 (GAS6), AXL stimulatory factor

<400> 41

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35 40 45

Ala Phe Gln Val Phe Glu Glu Ala Lys Gln Gly His Leu Glu Arg Glu
50 55 60

Cys Val Glu Glu Leu Cys Ser Arg Glu Glu Ala Arg Glu Val Phe Glu
65 70 75 80

Asn Asp Pro Glu Thr Asp Tyr Phe Tyr Pro Arg Tyr Leu Asp Cys Ile
85 90 95

Asn Lys Tyr Gly Ser Pro Tyr Thr Lys Asn Ser Gly Phe Ala Thr Cys
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Val Gln Asn Leu Pro Asp Gln Cys Thr Pro Asn Pro Cys Asp Arg Lys
115 120 125

Gly Thr Gln Ala Cys Gln Asp Leu Met Gly Asn Phe Phe Cys Leu Cys
130 135 140

Lys Ala Gly Trp Gly Gly Arg Leu Cys Asp Lys Asp Val Asn Glu Cys
145 150 155 160

Ser	Gln	Glu	Asn	Gly	Gly	Cys	Leu	Gln	Ile	Cys	His	Asn	Lys	Pro	Gly		
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Ser	Phe	His	Cys	Ser	Cys	His	Ser	Gly	Phe	Glu	Leu	Ser	Ser	Asp	Gly		
			180					185					190				
Arg	Thr	Cys	Gln	Asp	Ile	Asp	Glu	Cys	Ala	Asp	Ser	Glu	Ala	Cys	Gly		
		195					200					205					
Glu	Ala	Arg	Cys	Lys	Asn	Leu	Pro	Gly	Ser	Tyr	Ser	Cys	Leu	Cys	Asp		
	210					215					220						
Glu	Gly	Phe	Ala	Tyr	Ser	Ser	Gln	Glu	Lys	Ala	Cys	Arg	Asp	Val	Asp		
225					230					235					240		
Glu	Cys	Leu	Gln	Gly	Arg	Cys	Glu	Gln	Val	Cys	Val	Asn	Ser	Pro	Gly		
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			260					265					270				
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Pro	Val	Ile	Arg	Leu	Arg	Phe	Lys	Arg	Leu	Gln	Pro	Thr	Arg	Leu	Val		
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Ala	Glu	Phe	Asp	Phe	Arg	Thr	Phe	Asp	Pro	Glu	Gly	Ile	Leu	Leu	Phe		
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Ala	Gly	Gly	His	Gln	Asp	Ser	Thr	Trp	Ile	Val	Leu	Ala	Leu	Arg	Ala		
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Ser	Ser	Gly	Pro	Val	Ile	Asn	His	Gly	Met	Trp	Gln	Thr	Ile	Ser	Val		
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Glu	Glu	Leu	Ala	Arg	Asn	Leu	Val	Ile	Lys	Val	Asn	Arg	Asp	Ala	Val		
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			420					425					430				
Leu	Val	Gln	Pro	Ile	Asn	Pro	Arg	Leu	Asp	Gly	Cys	Met	Arg	Ser	Trp		
		435					440					445					
Asn	Trp	Leu	Asn	Gly	Glu	Asp	Thr	Thr	Ile	Gln	Glu	Thr	Val	Lys	Val		
	450					455					460						
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465					470					475					480		

Pro Gly Ser Gly Phe Ala Phe Tyr Ser Leu Asp Tyr Met Arg Thr Pro
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 Leu Asp Val Gly Thr Glu Ser Thr Trp Glu Val Glu Val Val Ala His
 500 505 510
 Ile Arg Pro Ala Ala Asp Thr Gly Val Leu Phe Ala Leu Trp Ala Pro
 515 520 525
 Asp Leu Arg Ala Val Pro Leu Ser Val Ala Leu Val Asp Tyr His Ser
 530 535 540
 Thr Lys Lys Leu Lys Lys Gln Leu Val Val Leu Ala Val Glu His Thr
 545 550 555 560
 Ala Leu Ala Leu Met Glu Ile Lys Val Cys Asp Gly Gln Glu His Val
 565 570 575
 Val Thr Val Ser Leu Arg Asp Gly Glu Ala Thr Leu Glu Val Asp Gly
 580 585 590
 Thr Arg Gly Gln Ser Glu Val Ser Ala Ala Gln Leu Gln Glu Arg Leu
 595 600 605
 Ala Val Leu Glu Arg His Leu Arg Ser Pro Val Leu Thr Phe Ala Gly
 610 615 620
 Gly Leu Pro Asp Val Pro Val Thr Ser Ala Pro Val Thr Ala Phe Tyr
 625 630 635 640
 Arg Gly Cys Met Thr Leu Glu Val Asn Arg Arg Leu Leu Asp Leu Asp
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:SRm160
 GH1-67-PCR-G3F1

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 <223> n = g, a, c or t

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<210> 43

<211> 9027

<212> DNA

<213> Homo sapiens

<220>

<223> serine/arginine repetitive matrix 2 (SRRM2) cDNA

<400> 43

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Val	Gln	Lys	Ala	Gln	Thr	Lys	Glu	Gln	Ala	Asp	Phe	Ala	Ile	Glu	Ala		
				405					410					415			
Leu	Ala	Lys	Ala	Thr	Tyr	Glu	Arg	Met	Phe	Arg	Trp	Leu	Val	Leu	Arg		
			420					425					430				
Ile	Asn	Lys	Ala	Leu	Asp	Lys	Thr	Lys	Arg	Gln	Gly	Ala	Ser	Phe	Ile		
		435					440					445					
Gly	Ile	Leu	Asp	Ile	Ala	Gly	Phe	Glu	Ile	Phe	Asp	Leu	Asn	Ser	Phe		
	450					455					460						
Glu	Gln	Leu	Cys	Ile	Asn	Tyr	Thr	Asn	Glu	Lys	Leu	Gln	Gln	Leu	Phe		
465					470					475					480		
Asn	His	Thr	Met	Phe	Ile	Leu	Glu	Gln	Glu	Glu	Tyr	Gln	Arg	Glu	Gly		
				485					490					495			
Ile	Glu	Trp	Asn	Phe	Ile	Asp	Phe	Gly	Leu	Asp	Leu	Gln	Pro	Cys	Ile		
			500					505					510				
Asp	Leu	Ile	Glu	Lys	Pro	Ala	Gly	Pro	Pro	Gly	Ile	Leu	Ala	Leu	Leu		
			515				520					525					
Asp	Glu	Glu	Cys	Trp	Phe	Pro	Lys	Ala	Thr	Asp	Lys	Ser	Phe	Val	Glu		
	530					535					540						
Lys	Val	Met	Gln	Glu	Gln	Gly	Thr	His	Pro	Lys	Phe	Gln	Lys	Pro	Lys		
545					550					555					560		
Gln	Leu	Lys	Asp	Lys	Ala	Asp	Phe	Cys	Ile	Ile	His	Tyr	Ala	Gly	Lys		
				565					570					575			
Val	Asp	Tyr	Lys	Ala	Asp	Glu	Trp	Leu	Met	Lys	Asn	Met	Asp	Pro	Leu		
			580					585					590				
Asn	Asp	Asn	Ile	Ala	Thr	Leu	Leu	His	Gln	Ser	Ser	Asp	Lys	Phe	Val		
		595					600					605					
Ser	Glu	Leu	Trp	Lys	Asp	Val	Asp	Arg	Ile	Ile	Gly	Leu	Asp	Gln	Val		
	610					615					620						
Ala	Gly	Met	Ser	Glu	Thr	Ala	Leu	Pro	Gly	Ala	Phe	Lys	Thr	Arg	Lys		
625					630					635					640		
Gly	Met	Phe	Arg	Thr	Val	Gly	Gln	Leu	Tyr	Lys	Glu	Gln	Leu	Ala	Lys		
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Leu	Met	Ala	Thr	Leu	Arg	Asn	Thr	Asn	Pro	Asn	Phe	Val	Arg	Cys	Ile		
			660					665					670				
Ile	Pro	Asn	His	Glu	Lys	Lys	Ala	Gly	Lys	Leu	Asp	Pro	His	Leu	Val		
		675					680					685					
Leu	Asp	Gln	Leu	Arg	Cys	Asn	Gly	Val	Leu	Glu	Gly	Ile	Arg	Ile	Cys		
	690					695					700						
Arg	Gln	Gly	Phe	Pro	Asn	Arg	Val	Val	Phe	Gln	Glu	Phe	Arg	Gln	Arg		
705					710					715					720		

Tyr	Glu	Ile	Leu	Thr	Pro	Asn	Ser	Ile	Pro	Lys	Gly	Phe	Met	Asp	Gly	
				725					730					735		
Lys	Gln	Ala	Cys	Val	Leu	Met	Ile	Lys	Ala	Leu	Glu	Leu	Asp	Ser	Asn	
			740					745					750			
Leu	Tyr	Arg	Ile	Gly	Gln	Ser	Lys	Val	Phe	Phe	Arg	Ala	Gly	Val	Leu	
		755					760					765				
Ala	His	Leu	Glu	Glu	Glu	Arg	Asp	Leu	Lys	Ile	Thr	Asp	Val	Ile	Ile	
	770					775					780					
Gly	Phe	Gln	Ala	Cys	Cys	Arg	Gly	Tyr	Leu	Ala	Arg	Lys	Ala	Phe	Ala	
785					790					795					800	
Lys	Arg	Gln	Gln	Gln	Leu	Thr	Ala	Met	Lys	Val	Leu	Gln	Arg	Asn	Cys	
			805						810					815		
Ala	Ala	Tyr	Leu	Lys	Leu	Arg	Asn	Trp	Gln	Trp	Trp	Arg	Leu	Phe	Thr	
		820					825						830			
Lys	Val	Lys	Pro	Leu	Leu	Gln	Val	Ser	Arg	Gln	Glu	Glu	Glu	Met	Met	
	835						840					845				
Ala	Lys	Glu	Glu	Glu	Leu	Val	Lys	Val	Arg	Glu	Lys	Gln	Leu	Ala	Ala	
	850					855					860					
Glu	Asn	Arg	Leu	Thr	Glu	Met	Glu	Thr	Leu	Gln	Ser	Gln	Leu	Met	Ala	
865					870					875					880	
Glu	Lys	Leu	Gln	Leu	Gln	Glu	Gln	Leu	Gln	Ala	Glu	Thr	Glu	Leu	Cys	
			885						890					895		
Ala	Glu	Ala	Glu	Glu	Leu	Arg	Ala	Arg	Leu	Thr	Ala	Lys	Lys	Gln	Glu	
		900						905						910		
Leu	Glu	Glu	Ile	Cys	His	Asp	Leu	Glu	Ala	Arg	Val	Glu	Glu	Glu	Glu	
	915						920					925				
Glu	Arg	Cys	Gln	His	Leu	Gln	Ala	Glu	Lys	Lys	Lys	Met	Gln	Gln	Asn	
	930					935					940					
Ile	Gln	Glu	Leu	Glu	Glu	Gln	Leu	Glu	Glu	Glu	Glu	Ser	Ala	Arg	Gln	
945					950					955					960	
Lys	Leu	Gln	Leu	Glu	Lys	Val	Thr	Thr	Glu	Ala	Lys	Leu	Lys	Lys	Leu	
			965						970					975		
Glu	Glu	Glu	Gln	Ile	Ile	Leu	Glu	Asp	Gln	Asn	Cys	Lys	Leu	Ala	Lys	
			980					985					990			
Glu	Lys	Lys	Leu	Leu	Glu	Asp	Arg	Ile	Ala	Glu	Phe	Thr	Thr	Asn	Leu	
	995					1000						1005				
Thr	Glu	Glu	Glu	Glu	Lys	Ser	Lys	Ser	Leu	Ala	Lys	Leu	Lys	Asn	Lys	
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His	Glu	Ala	Met	Ile	Thr	Asp	Leu	Glu	Glu	Arg	Leu	Arg	Arg	Glu	Glu	
1025					1030					1035					1040	

Lys Gln Arg Gln Glu Leu Glu Lys Thr Arg Arg Lys Leu Glu Gly Asp
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 Ser Thr Asp Leu Ser Asp Gln Ile Ala Glu Leu Gln Ala Gln Ile Ala
 1060 1065 1070
 Glu Leu Lys Met Gln Leu Ala Lys Lys Glu Glu Glu Leu Gln Ala Ala
 1075 1080 1085
 Leu Ala Arg Val Glu Glu Glu Ala Ala Gln Lys Asn Met Ala Leu Lys
 1090 1095 1100
 Lys Ile Arg Glu Leu Glu Ser Gln Ile Ser Glu Leu Gln Glu Asp Leu
 1105 1110 1115 1120
 Glu Ser Glu Arg Ala Ser Arg Asn Lys Ala Glu Lys Gln Lys Arg Asp
 1125 1130 1135
 Leu Gly Glu Glu Leu Glu Ala Leu Lys Thr Glu Leu Glu Asp Thr Leu
 1140 1145 1150
 Asp Ser Thr Ala Ala Gln Gln Glu Leu Arg Ser Lys Arg Glu Gln Glu
 1155 1160 1165
 Val Asn Ile Leu Lys Lys Thr Leu Glu Glu Glu Ala Lys Thr His Glu
 1170 1175 1180
 Ala Gln Ile Gln Glu Met Arg Gln Lys His Ser Gln Ala Val Glu Glu
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 Lys Ala Lys Gln Thr Leu Glu Asn Glu Arg Gly Glu Leu Ala Asn Glu
 1220 1225 1230
 Val Lys Val Leu Leu Gln Gly Lys Gly Asp Ser Glu His Lys Arg Lys
 1235 1240 1245
 Lys Val Glu Ala Gln Leu Gln Glu Leu Gln Val Lys Phe Asn Glu Gly
 1250 1255 1260
 Glu Arg Val Arg Thr Glu Leu Ala Asp Lys Val Thr Lys Leu Gln Val
 1265 1270 1275 1280
 Glu Leu Asp Asn Val Thr Gly Leu Leu Ser Gln Ser Asp Ser Lys Ser
 1285 1290 1295
 Ser Lys Leu Thr Lys Asp Phe Ser Ala Leu Glu Ser Gln Leu Gln Asp
 1300 1305 1310
 Thr Gln Glu Leu Leu Gln Glu Glu Asn Arg Gln Lys Leu Ser Leu Ser
 1315 1320 1325
 Thr Lys Leu Lys Gln Val Glu Asp Glu Lys Asn Ser Phe Arg Glu Gln
 1330 1335 1340
 Leu Glu Glu Glu Glu Glu Ala Lys His Asn Leu Glu Lys Gln Ile Ala
 1345 1350 1355 1360

Thr Leu His Ala Gln Val Ala Asp Met Lys Lys Lys Met Glu Asp Ser
 1365 1370 1375
 Val Gly Cys Leu Glu Thr Ala Glu Glu Val Lys Arg Lys Leu Gln Lys
 1380 1385 1390
 Asp Leu Glu Gly Leu Ser Gln Arg His Glu Glu Lys Val Ala Ala Tyr
 1395 1400 1405
 Asp Lys Leu Glu Lys Thr Lys Thr Arg Leu Gln Gln Glu Leu Asp Asp
 1410 1415 1420
 Leu Leu Val Asp Leu Asp His Gln Arg Gln Ser Ala Cys Asn Leu Glu
 1425 1430 1435 1440
 Lys Lys Gln Lys Lys Phe Asp Gln Leu Leu Ala Glu Glu Lys Thr Ile
 1445 1450 1455
 Ser Ala Lys Tyr Ala Glu Glu Arg Asp Arg Ala Glu Ala Glu Ala Arg
 1460 1465 1470
 Glu Lys Glu Thr Lys Ala Leu Ser Leu Ala Arg Ala Leu Glu Glu Ala
 1475 1480 1485
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 1490 1495 1500
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 Met Lys Thr Gln Leu Glu Glu Leu Glu Asp Glu Leu Gln Ala Thr Glu
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 Asp Ala Lys Leu Arg Leu Glu Val Asn Leu Gln Ala Met Lys Ala Gln
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 Phe Glu Arg Asp Leu Gln Gly Arg Asp Glu Gln Ser Glu Glu Lys Lys
 1570 1575 1580
 Lys Gln Leu Val Arg Gln Val Arg Glu Met Glu Ala Glu Leu Glu Asp
 1585 1590 1595 1600
 Glu Arg Lys Gln Arg Ser Met Ala Val Ala Ala Arg Lys Lys Leu Glu
 1605 1610 1615
 Met Asp Leu Lys Asp Leu Glu Ala His Ile Asp Ser Ala Asn Lys Asn
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 Arg Asp Glu Ala Ile Lys Gln Leu Arg Lys Leu Gln Ala Gln Met Lys
 1635 1640 1645
 Asp Cys Met Arg Glu Leu Asp Asp Thr Arg Ala Ser Arg Glu Glu Ile
 1650 1655 1660
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 1665 1670 1675 1680

Glu Met Ile Gln Leu Gln Glu Glu Leu Ala Ala Ala Glu Arg Ala Lys
 1685 1690 1695
 Arg Gln Ala Gln Gln Glu Arg Asp Glu Leu Ala Asp Glu Ile Ala Asn
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 Ser Ser Gly Lys Gly Ala Leu Ala Leu Glu Glu Lys Arg Arg Leu Glu
 1715 1720 1725
 Ala Arg Ile Ala Gln Leu Glu Glu Glu Leu Glu Glu Glu Gln Gly Asn
 1730 1735 1740
 Thr Glu Leu Ile Asn Asp Arg Leu Lys Lys Ala Asn Leu Gln Ile Asp
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 Gln Ile Asn Thr Asp Leu Asn Leu Glu Arg Ser His Ala Gln Lys Asn
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 1780 1785 1790
 Lys Leu Gln Glu Met Glu Gly Thr Val Lys Ser Lys Tyr Lys Ala Ser
 1795 1800 1805
 Ile Thr Ala Leu Glu Ala Lys Ile Ala Gln Leu Glu Glu Gln Leu Asp
 1810 1815 1820
 Asn Glu Thr Lys Glu Arg Gln Ala Ala Cys Lys Gln Val Arg Arg Thr
 1825 1830 1835 1840
 Glu Lys Lys Leu Lys Asp Val Leu Leu Gln Val Asp Asp Glu Arg Arg
 1845 1850 1855
 Asn Ala Glu Gln Tyr Lys Asp Gln Ala Asp Lys Ala Ser Thr Arg Leu
 1860 1865 1870
 Lys Gln Leu Lys Arg Gln Leu Glu Glu Ala Glu Glu Glu Ala Gln Arg
 1875 1880 1885
 Ala Asn Ala Ser Arg Arg Lys Leu Gln Arg Glu Leu Glu Asp Ala Thr
 1890 1895 1900
 Glu Thr Ala Asp Ala Met Asn Arg Glu Val Ser Ser Leu Lys Asn Lys
 1905 1910 1915 1920
 Leu Arg Arg Gly Asp Leu Pro Phe Val Val Pro Arg Arg Met Ala Arg
 1925 1930 1935
 Lys Gly Ala Gly Asp Gly Ser Asp Glu Glu Val Asp Gly Lys Ala Asp
 1940 1945 1950
 Gly Ala Glu Ala Lys Pro Ala Glu
 1955 1960

<210> 50
 <211> 287
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:calmodulin 2
GH1-84-PCR-G3F1

<400> 50

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ctcttttttt ttctttcccc tctttggccc ttaagacttt cattttgttc agaaccatgc 180
tgggctagct aaagggtggg gagagggaag atgggccccca ccacgctctc aagagaacgc 240
acctgcaata aaacagtctt gtcggccagc tgcccagggg acggcag 287
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<210> 51

<211> 2190

<212> DNA

<213> Homo sapiens

<220>

<223> calmodulin 2 (phosphorylase kinase, delta), clone
MGC:1447 cDNA

<400> 51

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gatccccgtg ctccggacac cccgggcctc gccatggctg accagctgac tgaggagcag 120
attgcagagt tcaaggaggc cttctccctc tttgacaagg atggagatgg cactatcacc 180
accaaggagt tggggacagt gatgagatcc ctgggacaga accccactga agcagagctg 240
caggatatga tcaatgaggt ggatgcagat gggaaacggga ccattgactt cccggagttc 300
ctgaccatga tggccagaaa gatgaaggac acagacagtg aggaggagat ccgagaggcg 360
ttccgtgtct ttgacaagga tgggaatggc tacatcagcg ccgcagagct gcgtcacgta 420
atgacgaacc tgggggagaa gctgaccgat gaggagggtg atgagatgat cagggagggt 480
gacatcgatg gagatggcca ggtcaattat gaagagtttg tacagatgat gactgcaaag 540
tgaaggcccc ccgggcagct ggcatgccc gttctcttga tctctctctt ctgcgcgcgcg 600
cactctctct tcaacactcc cctgcgtacc ccggttctag caaacaccaa ttgattgact 660
gagaatctga taaagcaaca aaagatttgt cccaagctgc atgattgctc tttctccttc 720
ttccctgagt ctctctccat gccctcatc tcttctttt gccctcgcct cttccatcca 780
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catcttattt tgggtgctgg ggtggctgcc agccctgtcc cgggacctgc tgggagggac 960
aagaggccct cccccaggca gaagagcatg ccttttgccg ttgcatgcaa ccagccctgt 1020
gattccacgt gcagatccca gcagcctggt ggggcagggg tgccaagaga ggcattccag 1080
aaggactgag ggggcgttga ggaattgtgg cggtgactgg atgtggccca ggaggggggtc 1140
gagggggcca actcacagaa ggggactgac agtgggcaac actcacatcc cactggctgc 1200
tgttctgaaa ccatctgatt ggctttctga ggtttggctg ggtggggact gctcatttgg 1260
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ttcagtcgtc tgggtttttt ccccttttct gtctatttca tctggctccc cccaccacct 1860
ccccacccca cccccaccc cctgcttccc ctcaactgcc aggtcgatca agtggtttt 1920
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gtgactacct gaaaaaaaaa aaaaaaaaaa 2190
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<210> 52
 <211> 149
 <212> PRT
 <213> Homo sapiens

<220>
 <223> calmodulin 2 (phosphorylase kinase, delta)

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 20 25 30
 Leu Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu
 35 40 45
 Leu Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile
 50 55 60
 Asp Phe Pro Glu Phe Leu Thr Met Met Ala Arg Lys Met Lys Asp Thr
 65 70 75 80
 Asp Ser Glu Glu Glu Ile Arg Glu Ala Phe Arg Val Phe Asp Lys Asp
 85 90 95
 Gly Asn Gly Tyr Ile Ser Ala Ala Glu Leu Arg His Val Met Thr Asn
 100 105 110
 Leu Gly Glu Lys Leu Thr Asp Glu Glu Val Asp Glu Met Ile Arg Glu
 115 120 125
 Ala Asp Ile Asp Gly Asp Gly Gln Val Asn Tyr Glu Glu Phe Val Gln
 130 135 140
 Met Met Thr Ala Lys
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<210> 53
 <211> 296
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: novel symporter
 GH1-178-PCR-G3F1

<400> 53
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 ccggccgggg gacccgagtg ggcgatcgcg gagcaggctg gggccagagg ccgcctccct 180
 tccggaggct ctcacctgcc acagccaccg ctgcaccgca ggaaccagc acagtgggta 240
 gattgataag cggccgctcg actagtctga ggtctgatac tcaactgactg tcgtat 296

<210> 54
 <211> 527
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: novel
semaphorin GH1-204-PCR-G3F1

<400> 54

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cacccccatt cctggacacg tggccctcc atctcaaacc tgcagtgggt gttaaaccct 180
tctcatgctt ctcatctcta cttcaggaat acagatagtg tctgggtggct tgacgtgatt 240
ttaatgaatt tggactccat gtggatttgg tegtctccct attccgagct gcgggcaggg 300
agaggggcct cgcgcgcgcc tcagcagccg gcggcggccg aggtagacga gcggggacgg 360
aaggacagac cgacgtcgcc agctggaatc atgtgagggc caaccgggga aggtggagca 420
gatgagcaca cacaggagcc gtctcctcac cgccgcccct ctcagcatgg aacagaggcg 480
ccctggcccc gggccctgga ggtggacagc cgctctgtgg tcctgct 527

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<210> 55

<211> 482

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: novel Zn finger
helicase GH1-31-PCR-G3F1

<400> 55

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aataaccgaa cacctggaag atggaccag cggttactat tcagcacaaa aaacatttct 120
gtgaaattgt gacaaacgtg gtcatttata aaaaaactgc cccttaccac gaaaagtctg 180
tcgtgtcttc ctgtgtcca ggagaggaca tctcctgtat tcctgttcag ccccccttg 240
cgaatactgt cctgtgccta atgtttgacc actcatgtct tttcagacat tcctggataa 300
acagtgtgac cgatgtcata ttgctaggca ctatacagat tcttgccaga aatcttgagg 360
cagttatcac cttacgacaa acttgaccac cccaaagccg aaaacctttc cgcaaaaacc 420
cgcacagtgg tttgattgat taaggcggcg ctcgactagt ctgaggtctg atactcactg 480
ac 482

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<210> 56

<211> 253

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: novel sugar
transporter GH1-175-PCR-G3F1

<400> 56

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gaggtgagct ggatgaacgg ctggctcagc tgccaggccc aggacgagat gctaaatttg 120
gccttcaactg tgggtcctt tctgctcagt gccatcacc tgcccctggg tatcgtcagt 180
gacaagtatg gcccaggaa gctcaggctg ctgggcagcg cctgcttcgc ggtttctctg 240
ttgctgattg cgt 253

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<210> 57

<211> 7554

<212> DNA

<213> Homo sapiens

<220>

<223> plexin-A2

<400> 57

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cggtagggcg tgcgagcgcc gcagccagcg gagcaaacct cgaaatagat ctggaaagcc 180
aggctcccgg aggaaatggg actgtgaacg aaccggagag caagaaggga aggaagcgcc 240
gggattgctg atgtcagagg agcccggaaa gtcgcgctgg aaaaatctga agacagccgg 300
ggctctgctt ctctctcagg agagacaccg ccggccgccc ccacacgccc cctcggcgcc 360
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gggtggcttga cgtggatttt aatgaatttg gactccatgt ggatttggtc gtctccctga 540
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<400> 58
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 35 40 45
 Thr Phe Asn His Leu Thr Val His Gln Gly Thr Gly Ala Val Tyr Val
 50 55 60
 Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr Gly Asn Leu Thr Ile Gln
 65 70 75 80
 Val Ala His Lys Thr Gly Pro Glu Glu Asp Asn Lys Ser Cys Tyr Pro
 85 90 95
 Pro Leu Ile Val Gln Pro Cys Ser Glu Val Leu Thr Leu Thr Asn Asn
 100 105 110
 Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser Glu Asn Arg Leu Leu Ala
 115 120 125
 Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys Leu Leu Arg Leu Asp Asp
 130 135 140
 Leu Phe Ile Leu Val Glu Pro Ser His Lys Lys Glu His Tyr Leu Ser
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 Ser Val Asn Lys Thr Gly Thr Met Tyr Gly Val Ile Val Arg Ser Glu
 165 170 175
 Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr Ala Val Asp Gly Lys Gln
 180 185 190
 Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys Leu Pro Arg Asp Pro Glu
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 Ser Ser Ala Met Leu Asp Tyr Glu Leu His Ser Asp Phe Val Ser Ser
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 Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala Leu Val Ser His Phe Asp
 225 230 235 240

Ile	Phe	Tyr	Ile	Tyr	Gly	Phe	Ala	Ser	Gly	Gly	Phe	Val	Tyr	Phe	Leu	245	250	255
Thr	Val	Gln	Pro	Glu	Thr	Pro	Glu	Gly	Val	Ala	Ile	Asn	Ser	Ala	Gly	260	265	270
Asp	Leu	Phe	Tyr	Thr	Ser	Arg	Ile	Val	Arg	Leu	Cys	Lys	Asp	Asp	Pro	275	280	285
Lys	Phe	His	Ser	Tyr	Val	Ser	Leu	Pro	Phe	Gly	Cys	Thr	Arg	Ala	Gly	290	295	300
Val	Glu	Tyr	Arg	Leu	Leu	Gln	Ala	Ala	Tyr	Leu	Ala	Lys	Pro	Gly	Asp	305	310	315
Ser	Leu	Ala	Gln	Ala	Phe	Asn	Ile	Thr	Ser	Gln	Asp	Asp	Val	Leu	Phe	325	330	335
Ala	Ile	Phe	Ser	Lys	Gly	Gln	Lys	Gln	Tyr	His	His	Pro	Pro	Asp	Asp	340	345	350
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Glu	Arg	Leu	Gln	Ser	Cys	Tyr	Gln	Gly	Glu	Gly	Asn	Leu	Glu	Leu	Asn	370	375	380
Trp	Leu	Leu	Gly	Lys	Asp	Val	Gln	Cys	Thr	Lys	Ala	Pro	Val	Pro	Ile	385	390	395
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His	Gly	Gly	Val	Gln	Tyr	Glu	Met	Val	Ser	Val	Leu	Lys	Asp	Gly	Ser	465	470	475
Pro	Ile	Leu	Arg	Asp	Met	Ala	Phe	Ser	Ile	Asp	Gln	Arg	Tyr	Leu	Tyr	485	490	495
Val	Met	Ser	Glu	Arg	Gln	Val	Thr	Arg	Val	Pro	Val	Glu	Ser	Cys	Glu	500	505	510
Gln	Tyr	Thr	Thr	Cys	Gly	Glu	Cys	Leu	Ser	Ser	Gly	Asp	Pro	His	Cys	515	520	525
Gly	Trp	Cys	Ala	Leu	His	Asn	Met	Cys	Ser	Arg	Arg	Asp	Lys	Cys	Gln	530	535	540
Gln	Ala	Trp	Glu	Pro	Asn	Arg	Phe	Ala	Ala	Ser	Ile	Ser	Gln	Cys	Val	545	550	555

Ser Leu Ala Val His Pro Ser Ser Ile Ser Val Ser Glu His Ser Arg
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 His Trp Cys Lys Tyr Arg Asn Leu Cys Thr His Asp Pro Thr Thr Cys
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 Tyr Glu Cys Val Leu Asn Ile Gln Gly Ala Ile His Arg Val Pro Ala
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 Leu Arg Phe Asn Ser Ser Ser Val Gln Cys Gln Asn Ser Ser Tyr Gln
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 Ser Ser His Asn Val Lys Cys Ser Asn Pro Gln Ile Thr Glu Ile Leu
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 Thr Val Ser Gly Pro Pro Glu Gly Gly Thr Arg Val Thr Ile His Gly
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Val	Asn	Leu	Gly	Leu	Asp	Phe	Ser	Glu	Ile	Ala	His	His	Val	Gln	Val	885	890	895
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Gln	Ile	Val	Cys	Glu	Met	Gly	His	Ala	Leu	Val	Gly	Thr	Thr	Ser	Gly	915	920	925
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Thr	Pro	Leu	Thr	Ile	Thr	Gly	Phe	Asn	Leu	Asp	Val	Ile	Gln	Glu	Pro	1060	1065	1070
Arg	Ile	Arg	Val	Lys	Phe	Asn	Gly	Lys	Glu	Ser	Val	Asn	Val	Cys	Lys	1075	1080	1085
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Asp	Tyr	Arg	Pro	Gly	Leu	Asp	Thr	Val	Glu	Arg	Pro	Asp	Glu	Phe	Gly	1105	1110	1115
Phe	Val	Phe	Asn	Asn	Val	Gln	Ser	Leu	Leu	Ile	Tyr	Asn	Asp	Thr	Lys	1125	1130	1135
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Val	Leu	Asp	Gln	Lys	Pro	Gly	Ser	Pro	Ile	Ile	Leu	Lys	Gly	Lys	Asn	1155	1160	1165
Leu	Cys	Pro	Pro	Ala	Ser	Gly	Gly	Ala	Lys	Leu	Asn	Tyr	Thr	Val	Leu	1170	1175	1180
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Cys Glu Pro Pro Asn Leu Thr Gly Gln His Lys Val Met Val His Val
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Tyr Lys Asn Val Pro Tyr Ser Gln Arg Pro Arg Ala Val Asp Met Asp	1540	1545	1550
Leu Glu Trp Arg Gln Gly Arg Ile Ala Arg Val Val Leu Gln Asp Glu	1555	1560	1565
Asp Ile Thr Thr Lys Ile Glu Gly Asp Trp Lys Arg Leu Asn Thr Leu	1570	1575	1580
Met His Tyr Gln Val Ser Asp Arg Ser Val Val Ala Leu Val Pro Lys	1585	1590	1595
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Pro Leu Arg Phe Trp Val Asn Val Ile Lys Asn Pro Gln Phe Val Phe	1745	1750	1755
Asp Ile His Lys Gly Ser Ile Thr Asp Ala Cys Leu Ser Val Val Ala	1765	1770	1775
Gln Thr Phe Met Asp Ser Cys Ser Thr Ser Glu His Arg Leu Gly Lys	1780	1785	1790
Asp Ser Pro Ser Asn Lys Leu Leu Tyr Ala Lys Asp Ile Pro Ser Tyr	1795	1800	1805
Lys Ser Trp Val Glu Arg Tyr Tyr Ala Asp Ile Ala Lys Leu Pro Ala	1810	1815	1820
Ile Ser Asp Gln Asp Met Asn Ala Tyr Leu Ala Glu Gln Ser Arg Leu	1825	1830	1835
			1840

His Ala Val Glu Phe Asn Met Leu Ser Ala Leu Asn Glu Ile Tyr Ser
 1845 1850 1855

Tyr Val Ser Lys Tyr Ser Glu Glu Leu Ile Gly Ala Leu Glu Gln Asp
 1860 1865 1870

Glu Gln Ala Arg Arg Gln Arg Leu Ala Tyr Lys Val Glu Gln Leu Ile
 1875 1880 1885

Asn Ala Met Ser Ile Glu Ser
 1890 1895

<210> 59
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 atcgtgaatt cagaaaacaa gattgtcggg attgggtaca atgggatgcc aaatgggtgc 180
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Glu Tyr Phe Met Ala Val Ala Phe Leu Ser Ala Gln Arg Ser Lys Asp
 20 25 30

Pro Asn Ser Gln Val Gly Ala Cys Ile Val Asn Ser Glu Asn Lys Ile
 35 40 45

Val Gly Ile Gly Tyr Asn Gly Met Pro Asn Gly Cys Ser Asp Asp Val
 50 55 60

Leu Pro Trp Arg Arg Thr Ala Glu Asn Lys Leu Asp Thr Lys Tyr Pro
 65 70 75 80

Tyr Val Cys His Ala Glu Leu Asn Ala Ile Met Asn Lys Asn Ser Thr
 85 90 95

Asp Val Lys Gly Cys Ser Met Tyr Val Ala Leu Phe Pro Cys Asn Glu
 100 105 110

Cys Ala Lys Leu Ile Ile Gln Ala Gly Ile Lys Glu Val Ile Phe Thr
 115 120 125

Ser Asp Lys Tyr His Asp Ser Asp Glu Ala Thr Ala Ala Arg Leu Leu
 130 135 140

Phe Asn Met Ala Gly Val Thr Phe Arg Lys Phe Ile Pro Lys Cys Ser
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Leu Gln

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<213> Artificial Sequence

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<210> 71
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